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We claim:

1. A method of repairing DNA double-strand breaks in vitro for forensic DNA genotyping, comprising the steps of:

(a) providing a forensic sample, comprising a non-supercoiled DNA molecule comprising a target region containing a DNA double-strand break;

(b) providing a pair of single-stranded DNA fragments, wherein the 3' end of the first fragment is homologous to at least 15 nucleotides of known sequence in the DNA molecule of step (a) and wherein sequence of the double strand break is within the targeting fragment;

(c) adding RecA protein or RecA protein homologue to the single-stranded DNA fragments;

(d) adding single-stranded binding protein (SSB) or SSB homologue;

(e) adding the DNA molecule of step (a) to the mixture resulting from step (d) and incubating until a strand invasion of the targeting fragments into the forensic DNA molecule has occurred; and

(f) adding DNA polymerase and dNTPs, wherein the proteins of steps (c) and (d) and the polymerase of step (f) are the only strand-repair proteins added to the system, and incubating the resulting mixture until the invading strand has extended, wherein the strand comprises sequences from the targeting fragment and the forensic DNA molecule of step (a).

2. The method of claim **1**, wherein the resulting extended DNA of step (f) is amplified and analyzed as part of a forensic DNA genotyping procedure.

3. The method of claim **1**, wherein the single-stranded DNA fragments have 15-2000 bp homology to the target region.

4. The method of claim **1**, wherein the single-stranded DNA fragments have 150-400 bp homology to the target region.

5. The method of claim **1**, wherein the single-stranded DNA of step (b) is directly synthesized or is converted from double-stranded targeting fragments.

6. The method of claim **1**, wherein the RecA protein and/or RecA homologue, SSB and/or SSB homologue, and DNA polymerase are from bacterial sources.

7. The method of claim **6**, wherein the bacterial source is *Escherichia coli*.

8. The method of claim **1**, wherein the DNA polymerase is selected from the group consisting of DNA polymerase I, DNA polymerase V, ϕ29 DNA polymerase and engineered translesion synthesis DNA polymerases.

9. The method of claim **1**, wherein step (c) is in the presence of a buffer for RecA protein or RecA homologue, containing an ATP regenerating system.

10. The method of claim **1**, wherein the target region is selected from the group consisting of autosomal short tandem repeat (STR), Y chromosome STR and mitochondrial DNA.

11. The method of claim **1**, wherein the target region is an autosomal STR selected from the group consisting of D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, D21S11, CSF1PO, FGA, Th01, TPOX, and VWA.

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